

ABSTRACT

A method is provided for assessing allelic losses and hypermethylation of genes in CpG tumor promotor region on specific chromosomal regions in cancer patients, including melanoma, neuroblastoma breast, colorectal, and prostate cancer patients.

- 5 The method relies on the evidence that free DNA and hypermethylation of genes in CpG tumor promotor region may be identified in the bone marrow, serum, plasma, and tumor tissue samples of cancer patients. Methods of melanoma, neuroblastoma, colorectal cancer, breast cancer and prostate cancer detection, staging, and prognosis are also provided.